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RAW SEQUENCE LISTING

DATE: 11/09/2001

PATENT APPLICATION: US/09/842,316

TIME: 07:39:24

Input Set : A:\Kostenis.txt

Output Set: N:\CRF3\11092001\I842316.raw

3 <110> APPLICANT: KOSTENSIS, Eva
 4 GASSENHUBER, Johann
 6 <120> TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
 8 <130> FILE REFERENCE: 38005-147
 10 <140> CURRENT APPLICATION NUMBER: US 09/842,316
 11 <141> CURRENT FILING DATE: 2001-04-26
 13 <150> PRIOR APPLICATION NUMBER: EP 116589.3
 14 <151> PRIOR FILING DATE: 2000-08-01
 16 <150> PRIOR APPLICATION NUMBER: EP 108858.2
 17 <151> PRIOR FILING DATE: 2000-04-26
 19 <160> NUMBER OF SEQ ID NOS: 9
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1197
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1194)
 31 <223> OTHER INFORMATION:
 34 <400> SEQUENCE: 1

35	atg gag tcg ggg ctg ctg cgg ccg gcg ccg gtg agc gag gtc atc gtc	48
36	Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val	
37	1 5 10 15	
39	ctg cat tac aac tac acc ggc aag ctc cgc ggt gcg cgc tac cag ccg	96
40	Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro	
41	20 25 30	
43	ggt gcc ggc ctg cgc gcc gac gcc gtg gtg tgc ctg gcg gtg tgc gcc	144
44	Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala	
45	35 40 45	
47	ttc atc gtg cta gag aat cta gcc gtg ttg ttg gtg ctc gga cgc cac	192
48	Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His	
49	50 55 60	
51	ccg cgc ttc cac gct ccc atg ttc ctg ctc ctg ggc agc ctc acg ttg	240
52	Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu	
53	65 70 75 80	
55	tcg gat ctg ctg gca ggc gcc gcc tac gcc gcc aac atc cta ctg tcg	288
56	Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser	
57	85 90 95	
59	ggg ccg ctc acg ctg aaa ctg tcc ccc gcg ctc tgg ttc gca cgg gag	336
60	Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu	
61	100 105 110	
63	gga ggc gtc ttc gtg gca ctc act gcg tcc gtg ctg agc ctc ctg gcc	384
64	Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala	
65	115 120 125	
67	atc gcg ctg gag cgc agc ctc acc atg gcg cgc agg ggg ccc gcg ccc	432
68	Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro	

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69	130	135	140	
71	gtc tcc agt cgg ggg cgc acg ctg gcg atg gca gcc gcg gcc tgg ggc	480		
72	Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly			
73	145 150 155 160			
75	gtg tcg ctg ctc ctc ggg ctc ctg cca gcg ctg ggc tgg aat tgc ctg	528		
76	Val Ser Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu			
77	165 170 175			
79	ggt cgc ctg gac gct tgc tcc act gtc ttg ccg ctc tac gcc aag gcc	576		
80	Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala			
81	180 185 190			
83	tac gtg ctc ttc tgc gtg ctc gcc ttc gtg ggc atc ctg gcc gct atc	624		
84	Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile			
85	195 200 205			
87	tgt gca ctc tac gcg cgc atc tac tgc cag gta cgc gcc aac gcg cgg	672		
88	Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg			
89	210 215 220			
91	cgc ctg ccg gca cgg ccc ggg act gcg ggg acc acc tcg acc cgg gcg	720		
92	Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala			
93	225 230 235 240			
95	cgt cgc aag ccg cgc tcg ctg gcc ttg ctg cgc acg ctc agc gtg gtg	768		
96	Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val			
97	245 250 255			
99	ctc ctg gcc ttt gtg gca tgt tgg ggc ccc ctc ttc ctg ctg ctg ttg	816		
100	Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu			
101	260 265 270			
103	ctc gac gtg gcg tgc ccg gcg cgc acc tgt cct gta ctc ctg cag gcc	864		
104	Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala			
105	275 280 285			
107	gat ccc ttc ctg gga ctg gcc atg gcc aac tca ctt ctg aac ccc atc	912		
108	Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile			
109	290 295 300			
111	atc tac acg ctc acc aac cgc gac ctg cgc cac gcg ctc ctg cgc ctg	960		
112	Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu			
113	305 310 315 320			
115	gtc tgc tgc gga cgc cac tcc tgc ggc aga gac ccg agt ggc tcc cag	1008		
116	Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln			
117	325 330 335			
119	cag tcg gcg agc gcg gct gag gct tcc ggg ggc ctg cgc cgc tgc ctg	1056		
120	Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu			
121	340 345 350			
123	ccc ccg ggc ctt gat ggg agc ttc agc ggc tcg gag cgc tca tcg ccc	1104		
124	Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro			
125	355 360 365			
127	cag cgc gac ggg ctg gac acc agc ggc tcc aca ggc agc ccc ggt gca	1152		
128	Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala			
129	370 375 380			
131	ccc aca gcc gcc cgg act ctg gta tca gaa ccg gct gca gac tga	1197		
132	Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp			
133	385 390 395			

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136 <210> SEQ ID NO: 2
137 <211> LENGTH: 398
138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapiens
141 <400> SEQUENCE: 2
143 Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
144 1 5 10 15
147 Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
148 20 25 30
151 Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
152 35 40 45
155 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
156 50 55 60
159 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
160 65 70 75 80
163 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
164 85 90 95
167 Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
168 100 105 110
171 Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala
172 115 120 125
175 Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
176 130 135 140
179 Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
180 145 150 155 160
183 Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
184 165 170 175
187 Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
188 180 185 190
191 Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
192 195 200 205
195 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
196 210 215 220
199 Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
200 225 230 235 240
203 Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
204 245 250 255
207 Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
208 260 265 270
211 Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
212 275 280 285
215 Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
216 290 295 300
219 Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
220 305 310 315 320
223 Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
224 325 330 335
227 Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
228 340 345 350

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231 Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
232          355          360          365
235 Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
236          370          375          380
239 Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
240 385          390          395
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 364
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 3
250 Met Ala Ala Ile Ser Thr Ser Ile Pro Val Ile Ser Gln Pro Gln Phe
251 1          5          10          15
254 Thr Ala Met Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
255          20          25          30
258 Phe Tyr Asn Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val
259          35          40          45
262 Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met
263          50          55          60
266 Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
267 65          70          75          80
270 His Phe Pro Ile Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
271          85          90          95
274 Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
275          100         105         110
278 Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
279          115         120         125
282 Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
283          130         135         140
286 Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
287 145          150         155         160
290 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
291          165         170         175
294 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
295          180         185         190
298 Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
299          195         200         205
302 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
303          210         215         220
306 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
307 225          230         235         240
310 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
311          245         250         255
314 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr
315          260         265         270
318 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
319          275         280         285
322 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
323          290         295         300

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326 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
327 305                               310           315           320
330 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly
331                               325           330           335
334 Pro Thr Glu Ser Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
335                               340           345           350
338 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
339                               355           360
342 <210> SEQ ID NO: 4
343 <211> LENGTH: 353
344 <212> TYPE: PRT
345 <213> ORGANISM: Homo sapiens
347 <400> SEQUENCE: 4
349 Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
350 1                               5           10           15
353 Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
354                               20           25           30
357 Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
358                               35           40           45
361 Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
362 50                               55           60
365 Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly
366 65                               70           75           80
369 Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
370                               85           90           95
373 Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
374                               100          105          110
377 Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
378                               115          120          125
381 Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
382 130                               135          140
385 Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
386 145                               150          155          160
389 Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
390                               165          170          175
393 Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
394                               180          185          190
397 Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
398 195                               200          205
401 Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
402 210                               215          220
405 Ser Gly Ser Ile Ser Arg Arg Thr Pro Met Lys Leu Met Lys Thr
406 225                               230          235          240
409 Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
410                               245          250          255
413 Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
414                               260          265          270
417 His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
418                               275          280          285

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VERIFICATION SUMMARY

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